

Application No.: 09/677,752
Amendment Dated: February 17, 2006
Reply to Office Action of: August 30, 2005

Attorney Docket No.: 71515.087.999
Customer No.: 35161

REMARKS

This Amendment is in response to the Office Action mailed on August 30, 2005, for the present application, which has been reviewed. Considered together with the following remarks, the arguments below and request for reconsideration are believed sufficient to place the application into condition for allowance. No new matter has been added to the application. Applicants express appreciation for the thoughtful examination by the Examiner.

Support for the amendments can be found in the specification as follows:

Amendment to claim 108: page 18, Table 1.
Amendment to claim 130: page 21, lines 20-34.

The present invention is drawn to PMP polypeptides of *Chlamydia*, further defined by amino acid and nucleotide sequences thereof, used in vaccine formulations comprising an effective amount of said polypeptide.

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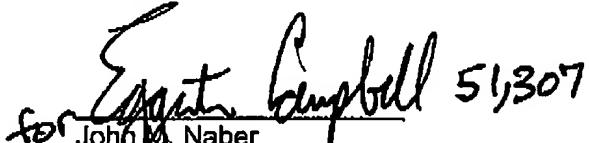
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CONCLUSION

In light of the foregoing, Applicants respectfully submit they have addressed each and every item presented by the Examiner in this Office Action. Favorable reconsideration of all of the claims as amended is earnestly solicited. Applicants submit that the present application, with the foregoing claim and specification amendments and accompanying remarks, is in a condition for allowance and respectfully request such allowance.

In the event any further matters requiring attention are noted by Examiner or in the event that prosecution of this application can otherwise be advanced thereby, a telephone call to Applicants' undersigned representative at the number shown below is invited.

Respectfully submitted,


for Egypt Campbell 51307
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DC 71515-87 108702v2 2/17/2006

Tuesday, September 8, 2003

Blast Result

Page 1



Blast 2 Sequences results

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.1 [Aug-1-2001]

Matrix **BLOSUM62** gap open: **11** gap extension: **1**
 χ_{dropoff} : **50** expect: **10.0** wordsize: **3** Filter Align

Sequence 1 **klseq_1** Length 956 (1 .. 956)Sequence 2 **klseq_2** Length 965 (1 .. 965)

(Score and expect value) is calculated based on the size of nr database.

Score = 1885 bits (4884), Expect = 0.0
 Identities = 925/934 (99%), Positives = 930/934 (99%)

Query: 23 VPDPTKESLSNKISLTGDTNL/TNCYLDNLRYILAILQKTPNEGAAVTITDYLSPFDTQK 82
 Sbjct: 32 VPDPTKESLSNKISLTGDTNL/TNCYLDNLRYILAILQKTPNEGAAVTITDYLSPFDTQK 91

Query: 63 EGIYFAKNLTPESGGAIYGASPNSPTVEIRDITGPVIFENNTCCRPTTSSNPNAAVNKR 142
 EGIYFAKNLTPESGGAIYGASPNSPTVEIRDITGPVIFENNTCCRPTTSSNPNAAVNKR 151

Query: 143 EGGAIHAQONLYINHNHDVVGFMNRFSYVRGGAISTANTFVUSENQSCFLFMDNICIQTNT 202
 EGGAIHAQONLYINHNHDVVGFMNRFSYVRGGAISTANTFVUSENQSCFLFMDNICIQTNT 211

Query: 203 AGKGQAIYAGTSNSFESNNCDLFFINNACCAAGGAIFSPICSLTGMRGNIVFYNNRCPIONV 262
 AGKGQAIYAGTSNSFESNNCDLFFINNACCAAGGAIFSPICSLTGMRGNIVFYNNRCPIONV 271

Query: 263 ETASSEASDGGAIKVTTRLDVTGNRGRIFFSDNITKNYGGAIYAPVVTLDNGPTYPINN 322
 ETASSEASDGGAIKVTTRLDVTGNRGRIFFSDNITKNYGGAIYAPVVTLDNGPTYPINN 331

Query: 323 VANNZGGAIYIDGTNSKISADRHAIIFNENIVTNVTSANGTSTSANFPRRNAITVASSS 382
 +ANIZGGAIYIDGTNSKISADRHAIIFNENIVTNVT+ANGTSTSANPPRRNAITVASSS 391

Query: 383 GEILLGAGGSQNLLIPYDPIEVSNAGVSFSNKEADQTGSVVPSGATVNSADPHORNLOTK 442
 GEILLGAGGSQNLLIPYDPIEVSNAGVSFSNKEADQTGSVVPSGATVNSADPHORNLOTK 451

Query: 443 TPAPLTLSNGFLCIEDHQAQLTVNRPQTGGVVS LGNGAVLSCYNGAGNSASMASITLKH 502
 TPAPLTLSNGFLCIEDHQAQLTVNRPQTGGVVS LGNGAVLSCYNGAGNSASMASITLKH 511

Query: 503 XGLNLSSILKSGAETPLMVEPTNNNNYTADTAATPSLSDVKLSLIDDYGNSPYESTDL 562

PAGE 16/18 * RCVD AT 2/17/2006 2:35:28 PM (Eastern Standard Time) * SVR:USPTO-EFXRF-6/36 * DNIS:2738300 * CSID:2026591559 * DURATION (mm:ss):04:48

day, September 6, 2001

Blast Result

Page: 2

bjct: 512 IGLNLSSILKSQAFIPLLWVPTNNSNNTADTAATFSISDVKLSLIDDYGNSPYESTDL 571
 query: 563 THALSSQFMLSISEASDNQLRSDDMDFSGLNVPHYGWQQLNSWGHAKTQDPPEPASSATIT 522
 THALSSQFMLSISEASDNQLRSDDMDFSGLNVPHYGWQQLM+NGNAXTQDPPEPASSATIT
 bjct: 572 THALSSQFMLSISEASDNQLRSDDMDFSGLNVPHYGWQQLMTWGWHAKTQDPPEPASSATIT 631
 query: 623 DPKKANRFHRTLLLTLWLPAGYVPSPKHRSPLIANTLWGNMLLATESLKNSAELTPSDHPP 682
 DP+KANRFHRTLLLTLWLPAGYVPSPKHRSPLIANTLWGNMLLATESLKNSAELTPSDHPP
 bjct: 632 DPKKANRFHRTLLLTLWLPAGYVPSPKHRSPLIANTLWGNMLLATESLKNSAELTPSDHPP 691
 query: 683 WGITGGGLGMMVYQEPRENHPGPFMHSGYPAGMIAQGQTHTPSLKFQSQTYTTLNERYARN 742
 WGITGGGLGMMVYQ+PRENHPGPFIHMRSSOY AGMIAGQTHPSLKFQSQTYTTLNERYARN
 bjct: 692 WGITGGGLGMMVYQDPRENHPGPFIHMRSSGYSAGMIAGQTHPSLKFQSQTYTTLNERYARN 751
 query: 743 NVSSKNYSCQGEMLFLSLQEGFLLAKLVGLSYGDHNCHFYTQGENLTSQGTFRSQTMGG 802
 NVSSKNYSCQGEMLFLSLQEGFLL KLVGLSYGDHNCHFYTQGENLTSQGTFRSQTMGG
 bjct: 752 NVSSKNYSCQGEMLFLSLQEGFLLTKLVGLSYGDHNCHFYTQGENLTSQGTFRSQTMGG 811
 query: 803 AVFFDLPNKPFGSTHILTAPFLGALGIYSSLSHFTEVGAYPRSFSTKPLINVLPVGVK 862
 AVFFDLPNKPFGSTHILTAPFLGALGIYSSLSHFTEVGAYPRSFSTKPLINVLPVGVK
 bjct: 812 AVFFDLPNKPFGSTHILTAPFLGALGIYSSLSHFTEVGAYPRSFSTKPLINVLPVGVK 871
 query: 863 GSFNMATQRQPQAWTVELAYQPVLVYRQEELIATQLLASKGIWFQSGSPSSRHAMSYKISQQ 922
 GSFMNATQRQPQAWTVELAYQPVLVYRQE IATQLLASKGIWFQSGSPSSRHAMSYKISQQ
 bjct: 872 GSFNMATQRQPQAWTVELAYQPVLVYRQEPCIATQLLASKGIWFQSGSPSSRHAMSYKISQQ 931

pu time: 0.36 user secs. 0.02 sys. secs 0.38 total secs.

apped		
ambda	K	H
0.316	0.132	0.396

apped		
ambda	K	H
0.267	0.0410	0.140

matrix: BLOSUM62
 gap Penalties: Existence: 11, Extension: 1
 number of hits to DB: 12,524
 number of Sequences: 0
 number of extensions: 873
 number of successful extensions: 15
 number of sequences better than 10.0: 1
 number of HSP's better than 10.0 without gapping: 1
 number of HSP's successfully gapped in prelim test: 0
 number of HSP's that attempted gapping in prelim test: 0
 number of HSP's gapped (non-prelim): 1
 length of query: 956
 length of database: 239,316,239
 effective HSP length: 131
 effective length of query: 825
 effective length of database: 206,923,009
 effective search space: 170381482425
 effective search space used: 170381482425
 r: 9
 A: 40
 X1: 16 (7.3 bits)
 X2: 129 (49.7 bits)
 X3: 129 (49.7 bits)
 S1: 41 (21.6 bits)
 S2: 77 (34.3 bits)